PDB ID or keyword C Author

Description

Classification

GO Terms

PF01370 🖾

PROTEIN (GDP-FUCOSE SYNTHETASE) (1FXS:A)

A MEMBER OF I

As of Tuesday Sep 02, 2008 there are 52821 Structures @ | Pl

Site Search ( ) Advanced Search

An Information Portal to Biological Macromolecular

TEIN DATA

CONTACT US I HELP | PRINT PAGE

Home Search Structure Results Queries

№ 1FXS

Download Files

譯 FASTA Sequence

Download Original Files

Display Files

Display Molecule

Structural Reports

S External Links

Structure Analysis

Having trouble with the web site? Try the tutorial click here Are you missing data updates? The PDB archive has moved to ftp://ftp.wwpdb.org. For more information click here. Help Structure Summary Biology & Chemistry Materials & Methods Sequence Details Geometry Images and Visualizati 1fxs 图 圖 ② DOI 10.2210/pdb1fxs/pdb < Biological Molecu Red - Derived Information Title GDP-FUCOSE SYNTHETASE FROM ESCHERICHIA COLI COMPLEX WITH NADP Authors Somers, W.S., Stahl, M.L., Sullivan, F.X. Somers, W.S., Stahl, M.L., Sullivan, F.X. (1998) GDP-fucose synthetase from Escherichia coli: structure of a unique member of the short-chain dehydrogenase/reductase family that catalyzes two distinct reactions at the same active site. Structure 6: 1601-1612 **Primary Citation** [Abstract] 🧐 Deposition 1998-09-01 Release 1999-08-26 History Display Options Experimental Type X-RAY DIFFRACTION Data N/A Method KING Imol WebMol Resolution(A) ê R-Value R-Free Space Group Parameters MBT SimpleViewer 2.30 0.163 (obs.) n/a P3,21 MBT Protein Worksh OuickPDB Length (Å) 104.20 104.20 75.10 All Images 120.00 Angles [\*] alpha 90.00 90.00 gamma Capable of displaying biologica Unit Cell

Polymer 1 Molecule PROTEIN (GDP-FUCOSE SYNTHETASE) Chains A

Epimerase

Molecular Function

catalytic activitycoenzyme binding

Asymmetric Unit Classification Oxidoreductase Source Polymer 1 Scientific Name Escherichia coli Common Name Bacteria Expression system Escherichia coli Related PDB Hd Details Entries 1BSV null Ligand Chemical Hapten Smulanty Ligand Structure Drug Strutarity Component NADP NICOTINAMIDE-ADENINE- $C_{21} H_{28} N_7 O_{17} P_3$ NAP B DINUCLEOTIDE PHOSPHATE SCOP Domain Info Superfamily Family Domain Classification GDP-4-keto-6-Tyrosine-dependent oxidoreductases deoxy-d-mannose epimerase/reductase Esche (GDP- fucose synthetase) NAD(P)-binding Rossmann-fold (version 1.71) NAD(P)-binding Rossmann-fold Alpha and beta proteins (a/b) d1fxsa\_ domains CATH Domain Class Architecture Topology Homology Classification NAD(P)-bindi Rossmann-lik 1fxsA01 Alpha Beta 3-Layer(aba) Sandwich Rossmann fold (version v3.1.0) UDP-galactose 4-epimerase; domain 1 UDP-galactor epimerase, d Alpha Beta Alpha-Beta Complex PFAM PEAM ID Chain PEAM Accession Description Clan ID

NAD dependent epimerase/dehydratase family

Family

· cellular metabolic process

⊕ RCSB P

NADP\_Rossm

Cellular Component

o none